

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula  
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Heller Ehrman White & McAuliffe  
(B) STREET: 4350 La Jolla Village Drive, 6th Floor  
(C) CITY: San Diego  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 92122

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

## (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/835,682  
(B) FILING DATE: 10-APR-1997  
(C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/695,191  
(B) FILING DATE: 07-AUG-1996  
(C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/682,080  
(B) FILING DATE: 15-JUL-1996  
(C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/629,822  
(B) FILING DATE: 10-APR-1996  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L  
(B) REGISTRATION NUMBER: 33,779  
(C) REFERENCE/DOCKET NUMBER: 24601-402I

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 858-450-8403  
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(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:  
 (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTNCCATGA	TTTAAAGTTT	60
TCTCGCCATA	TTCTTGGTCC	TACAGTGTGC	ATTTCCTCCAT	TTNCACGTT	TTNCAGTGAT	120
TTCGTCATTT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTC	AGTTTTCTCT	240
GCCATATTTT	ACGTCCTAAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTCCAG	GTCCTATAAT	GTGCATTTCT	CATTTNNCAC	GTTTTTCAGT	GATTTTCGTCA	360
TTTTTTCAAG	TCGGCAAGTG	GATGTTTCTC	ATTNNCCATG	ATTNCAAGT	TTCTTGNAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTAAAT	TTTCCACCTT	TCATTTTTC	CACGCCATAT	480
TTCATGTCCT	AAAGTGTATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTTCT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTTT	CACCTTTTTTC	ACTGATTTTC	TCATTTTTTC	600
AGTCGTCAAC	TGGATCTTTC	TAATTTTCCA	TGATTTTCAG	TTATCTTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTTCTA	AATTTTCCAA	CTTTTTCAAAT	TTTTCTCGAC	ATATTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTCACGT	TTTTTCAGTGA	TTTCGTCATT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTTT	CTTGCTATAT	TCCATGTCTT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTTC	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCCTT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTT	ACGTTTTTCA	GTAATTTCTT	CATTTTTTAA	GCCCTCAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTACCG	TCCTAAAGTG	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTTCTCAT	TTTTTCACGT	TTTCAGTGAA	TTC			1293

- (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1044 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:  
 (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAAAC	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTTGAA	GCTTCTTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTTCTA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
ACACTCTTTT	TTGTAGTATC	TGGAAGTGGA	CATTTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTTG	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTGTCT	AGCTTTGAGG	ATTTCGTTGG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTTCC	AGAAACTTCT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660
GGATGTGGAC	ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720

AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAACAGTGT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTTGA	AACACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
CATTCCCAGA	ATCTTGTGTT	TGATGTTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCCTTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2492 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGGTTCACCC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGGC	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCCTG	TTTTTCCTTC	AGCAATTTGT	CATTTTTTAA	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTGTG	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TGTCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTCTTGN	NTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTATTTG	CAAATATTTT	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCACCTC	1260
TTTTTGIGTAT	ATCTACCTTT	TGTGTCATTT	GTTAAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAAG	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAGTTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACTTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATTG	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCACAAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAA	GCATCGCTCA	GTCCCCTCC	TCCCTATTTT	TCTACAATAA	ACTCTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280
TTGAATTTAC	AGAACTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340

CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCCGAG GTGGCGGCTG 2400  
 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG 2460  
 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
  - (D) OTHER INFORMATION IL-2 signal sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT  
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT  
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5					10					15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
		35					40					45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TCT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
	50					55					60					
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
65					70				75					80		
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
				85					90					95		
TTA	CTT	GAT	CAT	TAC	AAA	TAT	CTT	ACT	GCA	TGG	TTG	AAC	TTC	TTA	ATT	336
Leu	Leu	Asp	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Leu	Asn	Phe	Leu	Ile	
			100					105					110			
TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
			115				120						125			
GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
	130					135					140					
CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
	145				150					155					160	
GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
				165					170					175		
ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
			180					185					190			
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624

Ile	Met	Arg	Lys	Leu	Glu	Pro	Glu	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro		
		195					200					205					
TTC	AAA	GAG	AAA	GGT	GAA	GTT	CGT	CGT	CCA	ACA	TTA	TCA	TGG	CCT	CGT	672	
Phe	Lys	Glu	Lys	Gly	Glu	Val	Arg	Arg	Pro	Thr	Leu	Ser	Trp	Pro	Arg		
	210					215					220						
GAA	ATC	CCG	TTA	GTA	AAA	GGT	GGT	AAA	CCT	GAC	GTT	GTA	CAA	ATT	GTT	720	
Glu	Ile	Pro	Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Gln	Ile	Val		
	225				230					235					240		
AGG	AAT	TAT	AAT	GCT	TAT	CTA	CGT	GCA	AGT	GAT	GAT	TTA	CCA	AAA	ATG	768	
Arg	Asn	Tyr	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met		
			245						250					255			
TTT	ATT	GAA	TCG	GAT	CCA	GGA	TTC	TTT	TCC	AAT	GCT	ATT	GTT	GAA	GGC	816	
Phe	Ile	Glu	Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly		
			260				265						270				
GCC	AAG	AAG	TTT	CCT	AAT	ACT	GAA	TTT	GTC	AAA	GTA	AAA	GGT	CTT	CAT	864	
Ala	Lys	Lys	Phe	Pro	Asn	Thr	Glu	Phe	Val	Lys	Val	Lys	Gly	Leu	His		
		275					280					285					
TTT	TCG	CAA	GAA	GAT	GCA	CCT	GAT	GAA	ATG	GGA	AAA	TAT	ATC	AAA	TCG	912	
Phe	Ser	Gln	Glu	Asp	Ala	Pro	Asp	Glu	Met	Gly	Lys	Tyr	Ile	Lys	Ser		
	290					295					300						
TTC	GTT	GAG	CGA	GTT	CTC	AAA	AAT	GAA	CAA	TAA						945	
Phe	Val	Glu	Arg	Val	Leu	Lys	Asn	Glu	Gln								
	305				310												

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC

30

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAAGTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	GACTGACACC	ATTAACACTT	TGTCAGCCTC	AGTGACTACA	GTCATAGATG	240
AACAGGCCTC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTTCA	GATACAACTA	GATGTATTAT	GACAAATAAC	TCAGCAGGGA	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATT	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAAG	TCTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGAATTT	GAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGGA	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAATTG	GATCTCCTCA	GCATTTTCTT	TCTTTAAAAA	ATGGGTGGGA	TTAATATTAT	600
TTGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGGTCTGT	AAGCTTAAGG	660
CCCAAACTAG	GAGAGACAAG	GTGGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGAG	TGTGCTTCAG	CAGCCCGAGA	840
GAGTTGCAAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTTCAT	GAAGGTTTCA	TGTCCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTCAGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCCTG	1020
TACATGGCTC	CTTTACCTAC	ACACTGGGGA	TTTGACCTCT	ATCTCCACTC	TCATTAATAT	1080
GGGTGGCCTA	TTTGCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GTTGGGAGCC	GCGCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTTCTAAGTG	GTAACAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GTGGTTCTTC	ACTCCATGTG	CTCTGCCTTC	CCCGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGACTGACAC	GTCTTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTCT	CTCTCTCTCT	TGCTTCTCTC	TCTTGCTTTT	TCGCTCTCTT	1380
GCTTCCCGTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAAGTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	ACAACATAGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240



TTCCGGGATT	GCGTGTATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTTGT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTTGAA	CAGATCCTTC	360
GGGAATTGAG	ACTTCAGGTC	AACTCCACGC	GCTTGGACCT	GTCCCTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTTCTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTTG	480
GAGATACACT	TTGCTGTGGA	TTAGTGTTC	TTCTTTGATT	GGTCTGTAAG	CTTAAGGCCC	540
AAACTAGGAG	AGACAAGGTG	GTTATTGCCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	600
CCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TCGCTGGCCA	CTCAGCTCTT	ATATCCCATG	660
AGGCTAGTCT	CATTGCACGG	GATAGAGTGA	GTGTGCTTCA	GCAGCCCGAG	AGAGTTGCAC	720
GGCTAAGCAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCATCTTTCA	AGAAGGTTGA	GTGTCCAAGT	GTCCTTCCTC	CAGGCAAAAC	GACACGGGAG	840
CAGGTCAGGG	TTGCTCTGGG	TAAAAGCCTG	TGAGCCTAAG	AGCTAATCCT	GTACATGGCT	900
CCTTTACCTA	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	960
ATTTGCTCTT	ATTAAAAGGA	AAGGGGGAGA	TGTTGGGAGC	CGCGCCCA	TTCGCCGTTA	1020
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGCGC	ATGCGCCGAG	1080
GGTGGTTCTT	CACTCCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCAATCA	GGGAGTACA	CGTCCTAGGC	GAAGGAAAAT	TCTCCTTAAT	AGGGACGGGG	1200
TTTCGTTTTT	TCTCTCTCTT	GCTTCGCTCT	CTCTTGCTTC	TTGCTCTCTT	TTCCTGAAGA	1260
TGTAAGAATA	AAGCTTTGCC	GCAGAAGATT	CTGGTCTGTG	GTGTTCTTCC	TGGCCGGTCG	1320
TGAGAACGCG	TCTAATAACA	ATTGGTGCCG	AAACCCGGGT	GATAATGATT	ATCATCTACA	1380
TATCACAAAC	TGCGTGGAGG					1400

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	ACTTTACGGG	TCCTTTTCACT	60
ACAAC TGCCA	CGAGGCCCCG	TGCTCTGGTA	ATAGATCTTT	GCTGAAAAGG	CACACACATG	120
ACACATTACT	CAAGGTGGGC	TCATCTGAGC	TGCAGATTCA	GCTTAATATG	AATCTTGCCA	180
ATTGTGTGAA	ATCATAAATC	TTCAAAGTGA	CACTCATTCG	CAGACACAGG	TGCCCACCTT	240
TGGCATAATA	AACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTTGAGAGCT	TAAATTTAAT	AAAGTGATAT	360
ACCTAATAAA	AATTAAATTA	AGAAGGTGTG	AATATACTAC	AGTAGGTAAA	TTATTTTCATT	420
AATTTATTTT	CTTTCTTAAT	CCTTTATAAT	GTTTTCTGCT	ATTGTCAATT	GCACATCCAT	480
ATGTTCAATT	CTTCACTGTA	ATGAAGAAAT	GTAGTAAATA	TACTTTCCGA	ACAAGTTGTA	540
TCAAATATGT	TACACTTGAT	TCCGTGTGTT	ACTTATCATT	TTATTATTAT	ATTGATTGCA	600
TTCCTTCGTT	ACTTGATATT	ATTACAAGGT	ACATATTTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACCAT	TTTATAACAT	ACTTTATTTA	TTCATTTCTT	ATGTGTGCTG	TGAGGCACAA	720
ATGCCAGAGA	GAACCTTGAGC	AGATAAGAGG	ACAAATTGCA	AGAGTCAGTT	ACCTCCTGCT	780
GTTCCCTTGA	AACTCAGGAT	CAAATTCAGG	TTGTCAGGCT	TGGCAGCATG	CACTTTTTAC	840
CAGTGCCCTCC	ATCTTGCTAG	CCCTGAACAT	CAAGCTTTGC	AGACAGACAG	GCTACACTAA	900
GTGAAC TGTT	CATTCACAGC	ATGCATGGTG	ATTTATTGTT	ACTTTCTATT	CCATGCCTTT	960
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTTTCGAGA	TAGAAGTTAC	TGAAAGAAAA	1020
TTACATTGTT	TTCTATAGAT	CCTTGATACT	CTTTCAGCAG	ATATAGAGTT	TTAATCAGGT	1080
CCTAGACCCT	TTCTTCACTC	TTATTAATAA	CTAAGTACAA	ATTAAGTTTA	TCCAAAACAG	1140
TACGGATGTT	GATTTTGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1200
CAC TTATTGG	GAATGTTTTT	GTTAATAAAA	GATTCAGGTG	TTACTCTAGG	TCAAGAGAAT	1260
ATTAAACATC	AGTCCCAAAT	TACAAACTTC	AATAAAAAGAT	TTGACTCTCC	AGTGGTGGCA	1320
ATATAAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACTG	GCGTGGAGG		1369

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTC	CCCT	ATCCCT	AAATC	CAGATT	GGT	GAATA	AACT	GTATAG	ATGT	TTGTG	CATTA	60
AAAAC	CCGT	AGGAT	CTTCA	CTCTAG	GTCA	CTGTT	CAGCA	CTGGA	ACCTG	AATTGT	GGGCC	120
CTGAGT	GATA	GGTCT	TGGGA	CATATG	CAGT	TCTGC	ACAGA	CAGAC	AGACA	GACAG	ACAGA	180
CAGAC	AGACA	GACAG	ACGTT	ACAAAC	AAAC	ACGTT	GAGCC	GTGTG	CCAAC	ACACAC	ACAA	240
ACACCA	CTCT	GGCCAT	AAATT	ATTGAG	GACG	TTGATTT	TATT	ATTCTG	TGTT	TGTGAG	TCTG	300
TCTGT	CTGTC	TGTCT	GTCTG	TCTGT	CTGTC	TATCA	AAACCA	AAAGAA	ACCA	AACAATT	ATG	360
CCTGC	CTGCC	TGCCT	TGCCTG	CCTAC	ACAGA	GAAAT	GATTT	CTTCA	ATCAA	TCTAAA	ACGA	420
CCTCCT	TAAGT	TTGCCT	TTTTT	TCTCTT	TCTT	TATCTT	TTTTT	TTTTT	TCTT	TCTT	CCCT	480
TCTTCT	CTT	CTTCTT	CCCT	CTTCTT	CCCT	CTTCTT	TCT	TTCTT	TCTT	CTTACT	TTCT	540
TTCTT	CTT	CTTACAT	TTA	TTCTT	TTTCAT	ACATAG	TTTC	TTAGT	GTAAG	CATCC	CTGAC	600
TGTCT	TGAAG	ACACTT	TGTA	GGCCT	CAATC	CTGTA	AAGAGC	CTTCCT	CTGC	TTTTCA	AATG	660
CTGGC	CATGAA	TGTTGT	TACCT	CACAT	TGACC	AGCTT	AGTCT	TCAAG	TCTGA	GTTACT	TGGAA	720
AGGAG	TTC	AGAAG	ACTGG	TTATAT	TTTTT	CATTAT	TATT	TGCAT	TTTTA	TTAAA	ATTTA	780
ATTTCA	CCCAA	AAGAAT	TTTAG	ACTGAC	CAAT	TCAGAG	TCTG	CCGTT	TAAAA	GCATA	AAGGAA	840
AAAGT	AGGAG	AAAAAC	GTGA	GGCTG	TCTGT	GGATG	GTGCA	GGCTG	CTTTA	GGGAG	CCTCG	900
TCACC	ATTCT	GCACTT	TGCAA	ACCGG	GCCAC	TAGA	ACCCG	TGAAG	GGAGA	AACCA	AAGCG	960
ACCTG	GAAAC	AATAGG	TACAC	ATGA	AGGCCA	GCCAC	CTCCA	TCTTG	TGTG	CGGGAG	TTC	1020
GTTAG	CAGAC	AAGATG	GGCTG	CCATG	CACAT	GTTGT	CTTTT	AGCTT	GGTGA	GGTCA	AAGTA	1080
CAACCG	AGTC	ACAGA	ACAAG	GAAGT	TATACA	CAGTG	AGTTC	CAGGT	CAGCC	AGAGT	TTTACA	1140
CAGAG	AAACC	ACATCT	TGAA	AAAAA	CAAAA	AAATA	AAATTA	AAATA	ATATA	ATTTA	AAAAAT	1200
TTAAA	AATAG	CCGGG	AGTGA	TGGCG	CATGT	CTTTA	ATCCC	AGCTC	TCTTC	AGGC	CAGAGAT	1260
GGGAG	GATTT	CTGAG	TTTGA	GGCAG	CCTG	GTCTG	CAAAAG	TGAGT	TCCAG	GACAG	TCAAG	1320
GCTAT	ACAGA	GAAAC	CCCTGT	CTTGAA	AAACT	AAACT	AAAT	AAACT	AAACT	AAACT	AAAAA	1380
AATATA	AAAT	AAAAA	TTTTA	AAGA	ATTTA	AAAAA	CTACA	GAAAT	CAAAC	ATAAG	CCCAC	1440
GAGAT	TGCAA	GTAAC	TGCAA	TCATAG	CAGA	AATAT	TATAC	ACAC	ACAC	ACAC	AGACTC	1500
TGTCAT	AAAA	TCCAAT	GTGC	CTTCAT	GATG	ATCAA	ATTTT	GATAG	TCACT	AGT	AGAA	1560
GAATCA	TATG	TCTG	AAAAA	AAAGC	CAGAA	CCTTT	TCTGC	TTTTG	TTTTT	TTTTG	CCCCA	1620
AGATAG	GGTT	TCTCT	CAGTG	TATCC	CTGGC	ATCC	CTGCCT	GGA	ACTT	CTCT	TAGTTT	1680
GGTAG	CCTCA	AACTC	AGAGA	GGTCT	CTCT	GCCTG	CCTGC	CTGC	CTGC	GCCTG	CCTGC	1740
CTGC	CTGC	GCCTG	CCTCA	CTTCT	TCTGC	CACCC	ACACA	ACCG	AGTC	CA	ACCTAG	1800
TTTAT	TTCT	TCTT	TTCT	TCTT	TTCT	TCTT	TTCT	CTT	TCTT	TTCT	TTCT	1860
CTTCT	TTCT	TTCT	TTCT	TTCT	TTCT	TTCT	TTCT	TTCT	TTCT	TTCT	TTCT	1920
TGCT	TATAG	TTT	TATTC	ATTAG	TTTTT	AATG	TAAAGT	TGTG	TTTTT	GTG	TCTAT	1980
TGCCT	TATAG	CCTG	CTTGCC	AGGAG	AGGGC	AACAG	AACTT	AGGAG	AAACC	ACCAT	GCAGC	2040
TCCTG	AGAAT	AAGT	GAAAAA	ACAAC	AAAAA	AAGG	AAATTC	TAAT	CACATA	GAATG	TAGAT	2100
ATATG	CCGAG	GCTGT	CAGAG	TGCTT	TTTTA	GGCTT	AGTGT	AAGTA	ATGAA	AATTG	TGTG	2160
TGTCT	TTTTAT	CCAA	ACACAG	AAGAG	AGGTG	GCTCG	GCTG	CATGT	CTGTT	GTCTG	CATGT	2220
AGACC	AGGCT	GGCTT	TGAAC	ACATTA	ATCT	GTCTG	CCTCT	GCTT	CCCTAA	TGCTG	CGATT	2280
AAAGG	CATGT	GCCAC	CACTG	CCCG	ACTGA	TTTCT	TCTTT	TTTTT	TTTTT	TGGAA	AAATAC	2340
CTTCT	TTTCT	TTTCT	TTTCT	CTCTT	TTCTT	CTTCT	TTCTT	TTCTT	TTCTT	TCTT	TTTTT	2400
TTTCT	TTTTT	TTTTT	TTTTT	TTTTT	TTTTT	TTTTT	TTTTT	TTTTT	TTTTT	TGTG	CTCCAC	2460
AATTG	CCCTCA	GCTCT	GTCTCT	AATTCT	CTTT	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	2520
CAGTAT	GTAT	GTAT	ATAT	TTAGA	AGAAA	TACTA	ATCCA	TTAAT	AACTC	TTTTT	TTCTTA	2580
AAATT	CATGT	CATTCT	TGTG	CCACA	AAAGT	AGTT	CCAGGA	CTTAC	CAGAG	AAAC	CCCTGTG	2640
TTCAA	ATTTT	TGTGT	TCAAG	GTCAC	CCCTGG	CTTAC	AAAGT	GAGTT	TCAAG	TCCG	ATAGGG	2700
CTACAC	AGAA	AAAC	CATATC	TCAGA	AAAAA	AAAAA	AGTTCC	AAAC	ACAC	ACAC	ACAC	2760
ACACAC	ACAC	ACAC	ACAC	ACAC	ACAC	ACAC	ACAC	CGCG	CCGCG	CGAT	GAGGGG	2820
AAGTC	GTGCC	TAA	AATAAAT	ATTTT	TCTGG	CCAA	AGTGAA	AGCAA	ATCAC	TATGA	AGAGG	2880
TACTC	CTAGA	AAAA	AATAAAT	ACAA	ACGGG	TTTT	TAAATCA	TTCC	AGCACT	GTTTT	AATTT	2940
AACTC	TGAAT	TTAGT	CTTGG	AAA	AGGGGG	GGGT	GTGGGT	GAGT	GAGGG	GAGCG	AGCAG	3000
ACGGG	CGGG	GTAG	AGTGT	TTAAA	AATGA	GACCT	AAATG	TGGT	TGGAACG	GAGGT	CGCCG	3060
ACCCA	AAGCG	GTAG	AGTGT	TTAAA	AATGA	GACCT	AAATG	TGGT	TGGAACG	GAGGT	CGCCG	3120
CCACC	CTCCT	CTTCC	ACTGC	TTAG	ATGCTC	CCTT	CCCCCT	ACTG	TGCTCC	CTTCC	CCCCCTAA	3180
CTGTG	CCTAA	CTGTG	CCTGT	TCCCT	CACCC	CGCTG	ATTCG	CCAGC	GCACGT	ACTTT	GACTT	

CAAGAACGAT	TTTGCCTGTT	TTCACCGCTC	CCTGTCATAC	TTTCGTTTTT	GGGTGCCCGA	3240
GTCTAGCCCG	TTCGCTATGT	TCGGGCGGGA	CGATGGGGAC	CGTTTTGTGCC	ACTCGGGAGA	3300
AGTGGTGGGT	GGGTACGCTG	CTCCGTCGTG	CGTGCGTGAG	TGCCGGAACC	TGAGCTCGGG	3360
AGACCCTCCG	GAGAGACAGA	ATGAGTGAGT	GAATGTGGCG	GCGCGTGACG	GATCTGTATT	3420
GGTTTTGTATG	GTTGATCGAG	ACCATTGTCTG	GGCGACACCT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTCCAGG	CCTCTCAGGT	TGGTGACACA	GGAGAGGGAA	GTGCCTGTGG	TGAGGCGACC	3540
AGGGTGACAG	GAGGCCGGGC	AAGCAGGCGG	GAGCGTCTCG	GAGATGGTGT	CGTGTTTAAG	3600
GACGGTCTCT	AACAAGGAGG	TCGTACAGGG	AGATGGCCAA	AGCAGACCGA	GTTGCTGTAC	3660
GCCCTTTTGG	GAAAAATGCT	AGGGTTGGTG	GCAACGTTAC	TAGGTCGACC	AGAAGGCTTA	3720
AGTCCTACCC	CCCCCCCCCT	TTTTTTTTTT	TTTCCTCCAG	AAGCCCTCTC	TTGTCCCCGT	3780
CACCGGGGGG	ACCGTACATC	TGAGGCCGAG	AGGACGCGAT	GGGCCCGGCT	TCCAAGCCGG	3840
TGTGGCTCGG	CCAGCTGGCG	CTTCGGGTCT	TTTTTTTTTT	TTTTTTTTTT	TTTTCTCTCA	3900
GAAGCCTTGT	CTGTCGCTGT	CACCGGGGGC	GCTGTACTTC	TGAGGCCGAG	AGGACGCGAT	3960
GGGCCCCGGC	TTCCAAGCCG	GTGTGGCTCG	GCCAGCTGGA	GCTTCGGGTC	TTTTTTTTTT	4020
TTTTTTTTTT	TTTTTTTCTC	CAGAAGCCTT	GTCTGTCTGT	GTCACCGGGG	GCGCTGTACT	4080
TCTGAGGCCG	AGAGGACGCG	ATGGGTCCGG	TTCCAAGCCG	ATGTGGCGGG	GCCAGCTGGA	4140
GCTTCGGGTT	TTTTTTTTTT	CTCCAGAAGC	CCTCTCTTGT	CCCCGTCACC	GGGGGCGCTG	4200
TACTTCTGAG	GCCGAGAGGA	CGTGATGGGC	CCGGGTTCCA	GGCGGATGTC	GCCCGGTCAG	4260
CTGGAGCTTT	GGATCTTTTT	TTTTTTTTTT	CCTCCAGAAG	CCCTCTCTTG	TCCCCGTCAC	4320
CGGGGGCACC	TTACATCTGA	GGGCGAGAGG	ACGTGATGGG	TCCGGCTTCC	AAGCCGATGT	4380
GCGGGGGCCA	GCTGGAGCTT	GGGCTTTTTT	TTTTTCTCTC	CAGAAGCCCT	CTCTTGTCCT	4440
CGTCACCGGG	GGCGCTGTAC	TTCTGAGGCC	GAGAGGACGT	GATGGGCCCC	GGTTCAGGC	4500
GGATGTCGCC	CGGTCACTGT	GAGCTTTGGA	TCATTTTTTT	TTTTCCCTCC	AGAAGCCCTC	4560
TCTTGTCCTC	GTCACCGGGG	GCACCGTACA	TCTGAGGCCG	AGAGGACACG	ATGGGCTCTG	4620
CTTCCAAGCC	GATGTGGCCC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	TTTTTCTCTC	4680
CAGAAGCCCT	GTCTGTCTGT	GTCACCCGGG	GCGCTGTACT	TCTGAGGCCG	AGAGGACGCG	4740
ATGGGCCCGG	CTTCCAAGCC	GGTGTGGCTC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	4800
TTTTTTTTTT	TTCTCTCAGA	AACCTTGTCT	GTCGCTGTCA	CCCGGGGCGC	TTGTACTTCT	4860
GATGCCGAGA	GGACGCGATG	GGCCCGTCTT	CCAGGCCGAT	GTGGCCCGGT	CAGCTGGAGC	4920
TTTGGATCTT	TTTTTTTTTT	TTTTCTCTCA	GAAGCCCTCT	CTTGTCCCCG	TCACCGGGGG	4980
CACCTTACAT	CTGAGGCCCTA	GAGGACACGA	TGGGCCCGGG	TTCCAGGCCG	ATGTGGCCCC	5040
GTCAGCTGGA	GCTTTGGATC	TTTTTTTTTT	TTTTCTCTCA	GAAGCCCTCT	TGTCCCCGTC	5100
ACCGTGCGCA	CTGTACATCT	GAGGCGGAGA	GGACATTATG	GGCCCGGCTT	CCAATCCGAT	5160
GTGGCCCGGT	CAGCTGGAGC	TTTGGATCTT	ATTTTTTTTT	TAATTTTTTT	TTCCAGAAGC	5220
CCTCTTGTC	CTGTACCCGG	TGGCACGGTA	CATCTGAGGC	CGAGAGGACA	TTATGGGCCC	5280
GGCTTCCAGG	CCGATGTGGC	CCGGTCAGCT	GGAGCTTTGG	ATCTTTTTTT	TTTTTTTTTCT	5340
TTTTTCTCTC	AGAAGCCCTC	TCTGTCCCTG	TCACCGGGGG	CCCTGTACGT	CTGAGGCCGA	5400
GGGAAAGCTA	TGGGCGCGGT	TTTCTTTTCT	TGACCTGTCT	GTCTTATCAG	TTCTCCGGGT	5460
TGTCAGGGTC	GACCATGTGT	TCCGTTGAGG	TCCGGTCTCT	TTTCGTTATG	GCTCATTTTT	5520
GGGCCACCTC	CCCAGGTATG	ACTTCCAGGC	GTCGTTGCTC	GCCTGTCACT	TTCTCCCTG	5580
TCTCTTTTAT	GCTTGTGATC	TTTCTATCT	GTTCTTATG	GACCTGGAGA	TAGGTACTGA	5640
CACGCTGTCC	TTTCCCTATT	AACACTAAAG	GACACTATAA	AGAGACCCTT	TCGATTTAAG	5700
GCTGTTTTTG	TTGTCCAGCC	TATTTCTTTT	ACTGGCTTGG	GTCTGTCTCG	GTGCTCTGAAG	5760
CTGTCCCCGA	GCCACGCTTC	CTGCTTTCCC	GGGCTTGCTG	CTTGCGTGTG	CTTGCTGTGG	5820
GCAGCTTGTG	ACAACCTGGG	GCTGTGACTT	TGCTGCGTGT	CAGACGTTTT	TCCCCGATTC	5880
CCCGAGGTGT	CGTTGTCACT	CCTGTCCCGG	TTGGAATGGT	GGAGCCAGCT	GTGGTTGAGG	5940
GCCACCTTAT	TTCCGGCTCAC	TTTTTTTTTT	TTTTTTTCTC	TTGGAGTCCC	GAACCTCCGC	6000
TCTTTTCTCT	TCCCGGTCTT	TCTTCCACAT	GCCTCCCGAG	TGCATTTCTT	TTTGTTTTTT	6060
TTCTTTTTTT	TTTTTTTTTT	TTGGGGAGGT	GGAGAGTCCC	GAGTACTTCA	CTCCTGTCTG	6120
TGGTGTCCAA	GTGTTTCATG	CACGTGCCTC	CCGAGTGCAC	TTTTTTTTTT	GGCAGTCGCT	6180
CGTTGTGTTT	TCTTGTCTGT	TGTCTGCCCC	TATCAGTAAC	TGTCTTGCCC	CGCGTGTAA	6240
ACATTCCTAT	CTCGCTTGT	TCTCCCGATT	GCGCGTCGTT	GCTCACTCTT	AGATCGATGT	6300
GGTGCTCCCG	AGTTCTCTTC	GGGCCAGGGC	CAAGCCGCGC	CAGGCGAGGG	ACGGACATTC	6360
ATGGCGAATG	GCGGCCGCTC	TTCTCGTTCT	GCCAGCGGGC	CCTCGTCTCT	CCACCCCATC	6420
CGTCTGCCCG	TGGTGTGTGG	AAGGCAGGGG	TGCGGCTCTC	CGGCCCGACG	CTGCCCCGCG	6480
CGCACTTTTC	TCAGTGGTTC	GCGTGTCTCT	TGTGGATGTG	TGAGGCGCCC	GGTTGTGCCC	6540
TCACGTGTTT	CACTTTGGTC	GTGTCTCGCT	TGACCATGTT	CCCAGAGTCG	GTGGATGTGG	6600
CCGGTGCGGT	TGCATACCCT	TCCGCTCTGG	TGTGTGCACG	CGCTGTTTCT	TGTAAGCGTC	6660
GAGGTGCTCC	TGGAGCGTTC	CAGGTTTGTG	TCCTAGGTGC	CTGCTTCTGA	GCTGGTGGTG	6720
GCGCTCCCCA	TTCCCTGGTG	TGCCCTCCGG	GCTCCGCTCT	GCTGTGTGCC	TTCCCGTTTG	6780
TGTCTGAGAA	GCCCGTGAGA	GGGGGGTCGA	GGAGAGAAAG	AGGGGCAAGA	CCCCCTTCT	6840
TCGTCCGGGT	AGGCGCCAC	CCCGGACTA	GTACGCTGT	GCGTAGGGCT	GGTGTGAGC	6900
GGTCGCGGCT	GGGGTTGGAA	AGTTTCTCGA	GAGACTCATT	GCTTTCCCGT	GGGGAGCTTT	6960
GAGAGGCCCTG	GCTTTCCGGG	GGGACCGGTT	GCAGGGTCTC	CCCTGTCCGC	GGATGCTCAG	7020
AATGCCCTTG	GAAGAGAACC	TTCTGTGTC	CGCAGACCCC	CCCGCGCGGT	CGCCCGCGTG	7080

TTGGTCTTCT GGTTTCCCTG TGTGCTCGTC GCATGCATCC TCTCTCGGTG GCCGGGGCTC 7140  
 GTCGGGGTTT TGGGTCCGTC CCGCCCTCAG TGAGAAAGTT TCCTTCTCTA GCTATCTTCC 7200  
 GGAAAGGGTG CGGGCTTCTT ACGGTCTCGA GGGGTCTCTC CCGAATGGTC CCCTGGAGGG 7260  
 CTCGCCCCCT GACCGCCTCC CGCGCGCGCA GCGTTTGCTC TCTCGTCTAC CGCGGCCCGC 7320  
 GGCTTCCCCG CTCCGAGTTC GGGGAGGGAT CACGCGGGGC AGAGCCTGTC TGTCTCTCTG 7380  
 CCGTTGCTGC GGAGCATGTG GCTCGGCTTG TGTGTTGGT GGCTGGGGAG AGGGCTCCGT 7440  
 GCACACCCCC GCGTGCGCGT ACTTTCTCTC CCTCCTGAGG GCCGCCGTGC GGACGGGGTG 7500  
 TGGGTAGGCG ACGGTGGGCT CCCGGGTCCC CACCCGTCTT CCCGTGCCTC ACCCGTGCCT 7560  
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 TGCTTTTTTT TTTCTCTGA GACAGTATTT CTCTGTGTAA CCTGGTGCCC TGAACCTAC 20760  
 TCTGTAGACC AGCCTGGCCT CAATCGAAT CAGAAATCCT CAGCTGGCAT TATTATCATT ATCATTATTA 20820  
 CAATTTTGGG GTAAAGGTGT GCTACACCAC GCTACGGCAT TATTATCATT ATCATTATTA 20880  
 ATTTTATTAT TAGACAGAAC GAAATCAACT AGTTGGTCCT GTTTCGTTAA TTCATTGAA 20940  
 ATTAGTTGGA CCAATTAGTT GGCTGGTTTG GGAGGTTTCT TTTGTTTCCG ATTTGGGTGT 21000  
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 GATTTTTTGA AAGATTACTT TTCTTAGTCT GAGGAAAAAA TAAAATAATA TTGGGCTACG 21120  
 TTTCAATTGCT TCATTTCTAT TTCTCTTTCT TTCTTTCTTT CTTTCAGATA AGGAGGTCGG 21180  
 CCAGTTCCCT CTGCCTTCTG GAAGATGTAG GCATTGCATT GGGAAAAGCA TTGTTTGAGA 21240  
 GATGTGCTAG TGAACCAGAG AGTTTGGATG TCAAGCCGTA TAATGTTTAT TACAATATAG 21300  
 AAAAGTTCTA ACAAAGTGAT CTTTAACTTT TTTTTTTTTT TTTCTCCTTC TACTTCTACT 21360  
 TGTCTCACT CTGCCACCAA CGCGCTTTGT ACATTGAATG TGAGCTTTGT TTTGCTTAAC 21420  
 AGACATATAT TTTTCTTTT GGTTTTGCTT GACATGGTTT CCCTTTCTAT CCGTGCAGGG 21480  
 TTCCAGACG GCCTTTTGAG AATAAAATGG GAGGCCAGAA CCAAAGTCTT TTGAATAAAG 21540  
 CACCACAAC CTAACTGT TGGCTGTTTT CCTTCCCAAG GCACAGATCT TTCCAGCAT 21600  
 GGAAAGCAT GTAGCAGTTG TAGGACACAC TAGACGAGAG CACCAGATCT CATTGTGGGT 21660  
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 TGAATGATCC CAGCATGGGA AGACAGTCTG CCTCTTTGT GGTATATCAC CATATACTCA 21840  
 ATAAATAAT GAAATGAAT AAGTCTCCAC GTATTTATTT CTTGAGCTA TCTAAATCT 21900  
 CTCACAGCAC CTCCCCCTCC CCCACACTGC CTTTCTCCCT ATGTTTGGGT GGGGCTGGGG 21960  
 GAGGGGTGGG GTGGGGGCGAG GGATCTGCAT GTCTTCTTGC AGGTCTGTGA ACTATTTGCG 22020  
 ATGGCCTGGT TCTCTGAAC GTTGAGCCTT GTCTATCCAG AGGCTGACTG GCTAGTTTTT 22080  
 TACCTGAAGT CCCTGAGTGA TGATTTCCCT GTGAATTC 22118

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42999 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCCTCTGG	CGACCTGTCTG	TCCGAGAGGT	TGGGCCTCCG	GATGCGCGCG	60
GGGCTCTGGC	CTCACGGTGA	CCGGCTAGCC	GGCCGCGCTC	CTGCCTTGAG	CCGCTTGCCG	120
CGCCCCGCGG	GCCTGTCTGT	CTCTCGCGCG	TCCGAGCGTC	CCGACTCCCG	GTGCCGGCCC	180
GGTCCCGGT	CTCTGACCCA	CCCGGGGGCG	GCGGGGAAGG	CGGCGAGGGC	CACCGTGCCC	240
CGTGCGCTCT	CCGCTGCGGG	CGCCCCGGGC	GCCGCACAAC	CCCACCCGCT	GGCTCCGTGC	300
CGTGCGTCTC	AGGCGTTCTC	GTCTCCGCGG	GGTTGTCCGC	CGCCCCCTTC	CCGGAGTGGG	360
GGTGGCCGG	AGCCGATCGG	CTCGCTGGCC	GGCCGGCCTC	CGCTCCCGGG	GGGCTCTTCG	420
ATCGATGTGG	TGACGTCTGT	CTCTCCCGGG	CCGGGTCCGA	GCCGCGACGG	GCGAGGGGCG	480
GACGTTCTGT	GCGAACGGGA	CCGTCTTTCT	CGCTCCGCCC	GCGCGGTCCC	CTCGTCTGCT	540
CCTCTCCCCG	CCCGCCGGCC	GGCGTGTGGG	AAGGCGTGGG	GTGCGGACCC	CGGCCCGACC	600
TCGCCGTCCC	GCCCCGCGCC	TTCGCTTCGC	GGGTGCGGGC	CGGCGGGGTC	CTCTGACGCG	660
GCAGACAGCC	TGCCTGTCTG	CCTCCAGTGG	TTGTTCGACTT	GCGGGCGGCC	CCCTCCGCG	720
GCGGTGGGGG	TGCCGTCCCC	CCGGCCCGTC	GTGCTGCCCT	CTCGGGGGGG	GTTTGC CGCA	780
GCGTCGGCTC	CGCCTGGGCC	CTTGCGGTGC	TCCTGGAGCG	CTCCGGGTTG	TCCCTCAGGT	840
GCCCCAGGCC	GAACGTTGGT	GTGTGCTTCC	CGCCCCCGGC	GCCCCCTCCT	CCGGTCGCGC	900
CCGCGGTGTC	CGCGCGTGGG	TCCTGAGGGA	GCTCGTCTGGT	GTGGGGTTTC	AGGCGGTTTG	960
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GGGTTCCGGC	CGGTGTGACG	CGTGCGCCGG	CCGGCCCGCG	AGGGGCTGCC	GTTCTGCCTC	1140
CGACCGGTCTG	TGTGTGGGTT	GACTTCGGAG	GCGCTCTGCC	TCGGAAGGAA	GGAGGTGGGT	1200
GGACGGGGGG	GCCTGGTGGG	GTTGCGCGCA	CGCGCGCACC	GGCCGGGGCC	CCGCCCTGAA	1260
CGCGAACGCT	CGAGGTGGCC	GCGCGCAGGT	GTTTCCTCGT	ACCGCAGGGC	CCCTCCCTT	1320
CCCCAGGCGT	CCCTCGGCGC	CTCTGCGGGC	CCGAGGAGGA	GCGGCTGGCG	GGTGGGGGGA	1380
GTGTGACCCA	CCCTCGGTGA	GAAAAGCCTT	CTCTAGCGAT	CTGAGAGGCG	TGCCTTGGGG	1440
GTACCGGATC	CCCCGGGCGC	CCGCCTCTGT	CTCTGCCTCC	GTTATGGTAG	CGCTGCCGTA	1500
GCGACCCGCT	CGCAGAGGAC	CCTCCTCCCG	TTCCCCCTCG	ACGGGGTTGG	GGGGGAGAAG	1560
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GCGCCTCCCC	CTTCCGAGTC	GGGGGAGGAT	CCCGCCGGGC	CGGGCCCGGC	GCTCCCACCC	1680
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CCCAGGCGGG	GCGCCGCGGG	ACCGCCCTCG	TGTCTGTGGC	GGTGGGATCC	CGCGGCGGTG	2100
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GCCGCCCGCC	GATCCTCTTC	TTCCCCCGGA	GCGGCTCACC	GGCTTCACGT	CCGTTGGTGG	2280
CCCCGCCTGG	GACCGAACCC	GGCACCGCCT	CGTGGGGCGC	CGCCGCCGGC	CACTGATCGG	2340
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GGCCCGGTGG	GCTTCCCGGA	GGGTTCGCGG	GGTCGGCCTG	CGGCGCGTGC	GGGGGAGGAG	2460
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TCGCCGAGGG	CCGTCGCGCC	GCCCCGGGTG	CCCCCGGGTG	CCGCCGGCGG	CGGTGAGGCC	2580
CCGCGCGTGT	GTCCCCGGTG	CGGTCGGGCC	CGCTCGAGGG	GTCCCCGTGG	CGTCCCCTTC	2640
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GGTCCCTCCC	GGACAGGCGT	TCGTGCGACG	TGTGGCGTGG	GTGACCTTCC	GCCTTGCCGG	2940
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TCGGCCGGGC	CCCGGGCCCT	CGACCGGACC	GGCTGCGCGG	GCGCTGCGGC	CGCACGGCGC	3180
GACTGTCCCC	GGGCCGGGCA	CCGCGTCCG	CCTCTCGCTC	GCCGCCCGGA	CGTCGGGGCC	3240
GCCCCGCGGG	GCGGGCGGAG	CGCGTCCCC	CGCTCGCCGC	CGCCCGCGGG	CGCCGGCCGC	3300
GCGCGCGCGC	GCGTGGCCGC	CGGTCCCTCC	CGGCCCGCCG	GCGCGGGTGC	GGCCGTCCGC	3360
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TGGTTGATCC	TGCCAGTAGC	ATATGCTTGT	CTCAAAGATT	AAGCCATGCA	TGTCTAAGTA	3720
CGCACGGCCG	GTACAGTGAA	ACTGCGAATG	GCTCATTAAA	TCAGTTATGG	TTCTTTTGGT	3780
CGCTCGCTCC	TCTCTACTTC	GGATAACTGT	GGTAATTCTA	GAGCTAATAC	ATGCCGACGG	3840
GCGCTGACCC	CCTTCGCGGG	GGGGATGCGT	GCATTTATCA	GATCAAAACC	AACCCGGTCA	3900
GCCCCCTCTC	GGCCCCGGCC	GGGGGGCGGG	CGCCGGCGGC	TTTGGTGACT	CTAGATAACC	3960
TCGGGCGCGAT	CGCACGCCCC	CCGTGGCGGG	GACGACCCAT	TCGAACGTCT	GCCCTATCAA	4020
CTTTCGATGG	TAGTCGCCGT	GCCTACCATG	GTGACCACGG	GTGACGGGGA	ATCAGGGTTC	4080
GATTCCGGAG	AGGGAGCCTG	AGAAACGGCT	ACCACATCCA	AGGAAGGCAG	CAGGCGCGCA	4140
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AGTCTGGTGC	CAGCAGCCGC	GGTAATTCCA	GCTCCAATAG	CGTATATTAA	AGTTGCTGCA	4320
GTTAAAAAGC	TCGTAGTTGG	ATCTTGGAAG	CGGGCGGGCG	GTCCGCCGCG	AGGCGAGCCA	4380
CCGCCCGTCC	CCGCCCTTGG	CCTCTCGGGC	CCCCCTCGAT	GCTCTTAGCT	GAGTGTCCCG	4440
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GGATACCGCA	GCTAGGAATA	ATGGAATAGG	ACCGCGGTTT	TATTTTGTGG	GTTTTTCGGAA	4560
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TTCTTGGACC	GGCGCAAGAG	GGACCAAGAG	GAAAGCAATT	GCCAAGAATG	TTTTTCATTAA	4680
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CGGAAGGGCA	CCACCAGGAG	TGGAGCCTGC	GGCTTAATTT	GACTCAACAC	GGGAAACCTC	4920
ACCCGCGCCG	GACACGGAGA	GGATTGACAG	ATTGATAGCT	CTTTCTCGAT	TCCGTGGGTG	4980
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TAGAGGGACA	AGTGGCGTTC	AGCCACCCGA	GATTGAGCAA	TAACAGGTCT	GTGATGCCCT	5160
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CGGCAGGCGC	GGGTAACCCG	TTGAACCCCA	TTCGTGATGG	GGATCGGGGA	TTGCAATTAT	5280
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GCGCCCCGCG	CCGTGGGGGC	GGGAACCCCC	GGGCGCCTGT	GGGGTGGTGT	CCGCGCTCGC	6420
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CCGGTCCCCT	TTGCTGTCTC	GTCTGGCCGG	CCTGAGGCAA	CCCCCTCTCC	TCTTGGGCGG	6540
GGGGGGCGGG	GGGACGTGCC	GCGCCAGGAA	GGGCCTCCTC	CCGGTGCCTC	GTGCGGAGCG	6600
CCCTCGCCAA	ATCGACCTCG	TACGACTCTT	AGCGGTGGAT	CACTCGGCTC	GTGCGTCTGAT	6660
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CCGATCAATC	GCCCCGGGGG	TGCCTCCGGG	CTCCTCGGGG	TGCGCGGCTG	GGGGTTCCTT	6840
GCGAGGGCCC	CTCCGTCCCC	CTCCGTCCCC	CTAAGCGCAG	ACCCGGGGCG	GTCCGCCCTC	6900
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ATGGTCTCGA	TCTCCTGACC	CCGTGATCCG	TCCACCTCGG	CCTCCCAAAG	TGCTGGGATG	37200
ACAGGCGTGA	GCCACCGGCC	CCGGCCTATT	TATCTATTTA	TTAACTTTGA	GTCCAGGTTA	37260
TGAAACCAGT	TAGTTTTTGT	AAATTTTTTT	TTTTTTTTTT	TTTTTTGAGA	CGAGGTTTCA	37320
CCGTGTTGCC	AAGGCTTGGA	CCGAGGGATC	CACCGGCCCT	CGGCCTCCCA	AAAGTGCGGG	37380
GATGACAGGC	GCGAGCCTAC	CGCGCCCGGA	CCCCCCTTTT	CCCCTTCCCC	CGCTTGTCTT	37440
CCCGACAGAC	AGTTTCACGG	CAGAGCGTTT	GGCTGGCGTG	CTTAAACTCA	TTCTAAATAG	37500
AAATTTGGGA	CGTCAGCTTC	TGGCCTCACG	GACTCTGAGC	CGAGGAGTCC	CCTGGTCTGT	37560
CTATCACAGG	ACCGTACACG	TAAGGAGGAG	AAAAATCGTA	ACGTTCAAAG	TCAGTCATTT	37620
TGTGATACAG	AAATACACGG	ATTCACCCAA	AACACAGAAA	CCAGTCTTTT	AGAAATGGCC	37680
TTAGCCCTGG	TGTCCTGTGC	AGTGATTCTT	TTCCGTTTGG	ACCTTGACTG	AGAGGATTCC	37740
CAGTCGGTCT	CTCGTCTCTG	GACGGAAGTT	CCAGATGATC	CGATGGGTGG	GGGACTTAGG	37800
CTGCGTCCCC	CCAGGAGCCC	TGGTCGATTA	GTTGTGGGGA	TCGCCTTGGA	GGGCGCGGTG	37860
ACCCACTGTG	CTGTGGGAGC	CTCCATCCTT	CCCCCACCCT	CCTCCCCAGG	GGGATCCCAA	37920
TTCAATCCGG	GCTGACACGC	TCAGTGGCAG	GCGTCGGGCA	TCACCTAGCG	GTCAGTGTTA	37980
CTCTGAAAAC	GGAGGCCTCA	GAGCACCAGG	GAGCACCAGG	CCGCCTGCGC	ACAGCCTGGG	38040
GCAACTGTGT	CTTCTCCACC	GCCCCCGCCC	CCACCTCCAA	GTTCTCTCCT	CCCTTGTTGC	38100
CTAGGAAATC	GCCACTTTGA	CGACCGGGTC	TGATTGACCT	TTGATCAGGC	AAAAACGAAC	38160
AAACAGATAA	ATAAATAAAA	TAACACAAAA	GTAACATACT	AAATAAAAATA	AGTCAATACA	38220
ACCCATTACA	ATACAATAAG	ATACGATACG	ATAGGATGCG	ATAGGATACG	ATAGGATACA	38280
ATACAATAGG	ATACGAATAC	ATACAATACA	ATACAATACA	ATACAATACA	ATACAATACA	38340
ATACAATACA	ATACAATACG	CCGGGCGCGG	TGGCTCATGC	CTGTCATCCC	GTCACTTTGG	38400
GATGCCGAGG	TGGACGCATC	ACCTGAAGTC	GGGAGTTGGA	GACAAGCCCG	ACCAACATGG	38460
AGAAATCCCC	TCTCAATTGA	AAATACAAAA	CTAGCCGGGC	GCGGTGGCAC	ATGCCTATAA	38520

TCCCAGCTGC	TAGGAAGGCT	GAGGCAGGAG	AATCGCTTGA	ACCTGGGAAG	CGGAGGTTGC	38580
AGTGAGCCGA	GATTGCGCCA	TCGCACTCCA	GTCTGAGCAA	CAAGAGCGAA	ACTCCGTCTC	38640
AAAAATAAAT	ACATAAATAA	ATACATACAT	ACATACATAC	ATACATACAT	ACATACATAC	38700
ATAAATTAAT	ATAAATTAAT	AAAATAAAAT	AAATAAATGG	GCCCTGCGCG	GTGGCTCAAG	38760
CCTGTCATCC	CCTCACTTTG	GGAGGCCAAG	GCCGGTGGAT	CAAGAGGCGG	TCAGACCAAC	38820
AGGGCCAGTA	TGGTGAAACC	CCGTCTCTAC	TCACAATACA	CAACATTAGC	CGGGCGCTGT	38880
GCTGTGCTGT	ACTGTCTGTA	ATCCCAGCTA	CTCGGGAGGC	CGAGCTGAGG	CAGGAGAATC	38940
GCTTGAACCT	GGGAGGCGGA	GGTTGCAGTG	AGCCGAGATC	GCGCCACTGC	AACCCAGCCT	39000
GGGCGACAGA	GCGAGACTCC	GTCTCCAAAA	AATGAAAAATG	AAAATGAAAC	GCAACAAAAAT	39060
AATTA AAAAG	TGAGTTTCTG	GGGAAAAAGA	AGAAAAAGAAA	AAAGAAAAAA	ACAACAAAAAC	39120
AGAACAACCC	CACCGTGACA	TACACGTACG	CTTCTCGCCT	TTCGAGGCCT	CAAACACGTT	39180
AGGAATTATG	CGTGATTTCT	TTTTTTAACT	TCATTTTATG	TTATTATCAT	GATTGATGTT	39240
TCGAGACGGA	GTCTCGGAGG	CCCGCCCTCC	CTGGTTGCCC	AGACAACCCC	GGGAGACAGA	39300
CCCTGGCTGG	GCCCCGATTGT	TCTTCTCCTT	GGTCAGGGGT	TTCTTTGTCT	TTCTTTCGTGT	39360
CTTTAACCCT	CGTGGACTCT	TCCGCCTCGG	GTTTGACAGA	TGGCAGCTCC	ACTTTAGGCC	39420
TTGTTGTTGT	TGGGGACTTT	CCTGATTCTC	CCCAGATGTA	GTGAAAGCAG	GTAGATTGCC	39480
TTGCCTGGCC	TTGCCTGGCC	TTGCCTTTTC	TTTCTTTCTT	TCTTTCTTTA	TTACTTTCTC	39540
TTTTTCTTCT	TCTTCTTCTT	CTTTTPTTTG	AGACAGAGTT	TCACTCTTGT	TGCCCAGGCT	39600
AGAGGGCAAT	GGCGCGATCT	CGGCTCACCG	CACCCCTCCGC	CTCCCAGGTT	CAAGCGATTG	39660
TCCTGCCTCA	GCCTCCTGAT	TAGCTGGGAT	TACAGGCATG	GGCCACCGTG	CTGGCTGATG	39720
TTTGTA CTTT	TAGTAGAGAC	GGTGTTTTTC	CATGTTGGTC	AGGCTGGTCT	CCCACTCCCA	39780
ACCTCAGGTG	GTCCGCCTGC	CTTAGCCTCC	CAAAGTGCTG	GGATGACAGG	CGTGCAACCG	39840
CGCCCAGCCT	CTCTCTCTCT	CTCTCTCTCT	CTCGCTCGCT	TGCTTGCTTG	CTTTCGTGCT	39900
TTCTTGCTTT	CCCGTTTTCT	TGCTTTCTTT	CTTCTTTTCG	TTTCTTTTCAT	GCTTGCTTTT	39960
TTGCTTGCTT	GCTTGCTTTT	GTGCTTTCTT	CTTCTCTGT	TTTCTTTCTT	TCTTTCTTTT	40020
TTTCTTTCTT	TTGTTTCTTT	CTTGCTTGCT	TTCTTGCTTG	CTTGCTTGCT	TTCTTGCTTT	40080
CTTGCTTTCC	TGTTTCTTTT	CTTCTTTCTT	TTCTTTCTTT	TCTTTCTTGC	TTGCTTTTCT	40140
GCTTGCTTGC	TTTCGTGCTT	TCTTGTTTTT	TCGATTTCTT	TCTTTCTTTT	GTTTTCTTTT	40200
TGCTTGCTTT	CTTGCTTGCT	TGCTTTCTGT	CTTCTTGCTT	TCCTGTTTTT	TTTCTTTCTT	40260
TCTTTCTTTT	GTCTTCTTCT	TGCTTGCTTT	CTTCTTGCTT	TGCTTTCTGT	CTGTCTTGTT	40320
TCTCGATTTT	TTTCTTTCTT	TTGTTTCTTT	CCTGCTTGCT	TTCTTGCTTG	ATTGCTTTCT	40380
TGCTTTCTTG	CTTCTTGCTT	TTCTTTCTTT	CTTTTGTTTT	TTTCTTTCTT	GCTTCTTGTT	40440
TTTCTTGCTT	TCTTGCTTGC	TTGCTTTCTG	GTCTTTCTGT	TTTCTTGCTT	TCTTTCTTTT	40500
GTTTCTTTCT	TGCTTGCTTT	CTTGCTTCTT	TGCTTTCTTG	CTTTCTTGCT	TGCTTGCTTT	40560
CGTGCTTTCT	TTCTTGCTTT	CTTTTCTTTT	TTTCTTTTCT	TTTTCTTTCT	TTCTTGCTTT	40620
CTTTTCTTTT	ATCATCATCT	TTCTTTCTTT	CCTTTCTTTT	TTTCTTTCTT	TCTATCTTTT	40680
TTTCTTTCTT	TCTTTCTTTT	TTTCTTTCTT	TCTTTCTGTT	TCGTCCTTTT	GAGACAGAGT	40740
TTCACTCTTG	TTTCCACGGC	TAGAGTGCAA	TGGCGCGATC	TTGGCTCACC	GCACCTTCCG	40800
CCTCCCGGCT	TCGAGCGCTT	CTCCTGCCTC	CAGCCTCCCG	ATTAGCGGGG	ATTGACAGGG	40860
AGGCACCCCT	ACGCCTGGCT	TGGCTGATGT	TTGTGTTTTT	AGTAGGCACG	CCGTGTCTCT	40920
CCATGTTGCT	CAGGCTGGTC	TCCAACCTCC	GACCTCCTGT	GATGCGCCCA	CCTCGGCCCT	40980
TCGAAGTGCT	GGGATGACGG	GCGTGACGAC	CGTGCCCGGC	CTGTTGACTC	ATTTTCGCTT	41040
TTATATTCTT	TCGTTTCCAC	TCGTTTACTT	ATATGTTATTA	ATGTAAACGT	TTCTGTACGC	41100
TTATATGCAA	ACAACGACAA	CGTGTATCTC	TGCATTTGAAT	ACTCTTGCGT	ATGGTAAATA	41160
CGTATCGGTT	GTATGGAAT	AGACTTCTGT	ATGATAGATG	TAGGTGTCTG	TGTTATACAA	41220
ATAAATACAC	ATCGCTCTAT	AAAGAAGGGA	TCGTCGATAA	AGACGTTTAT	TTTACGTATG	41280
AAAAGCGTCG	TATTTATGTG	TGTAAATGAA	CCGAGCGTAC	GTAGTTATCT	CTGTTTTCTT	41340
TCTTCTCTCT	CTTCGTGTTT	TTCTTCTTCT	TTCTTCTCCT	TTCTTCTCCT	CTTTAGGTTT	41400
TTCTTCTCTT	CTTCTTTTCT	TTCTTTCTCT	CTTTCTGTCT	TTTTTTCTCT	CGTGCTTTAT	41460
TTCTTCTTCT	TTCCCTGTGT	TTCTTCTTTT	TTTCTTTTCT	CTCTGTTTCT	TTTTCCCTTC	41520
TTTCTTCTCT	TTCTTTCTCT	ATTCTTTCTC	TCTTTTTCTG	TGTTTTCTTT	CTTCCCGTCT	41580
GTCTTTTAAA	AAATTGGAGT	GTTTCAGAAG	TTTACTTTGT	GTATCTACGT	TTTCTAAAT	41640
GTCTCTCTTT	TCTCCATTTT	CTTCTCTCCT	CCCTCCCTCC	CTCCCTGCTC	CCTTCCCTCC	41700
CTCCTTCCCT	TTCGCCATCT	GTCTCTTTTCT	CCCACTCCCC	TCCCCCGCTC	TGTCTCTGCG	41760
TGGATTCCGG	AAGAGCCTAC	CGATTCTGCC	TCTCCGTGTG	TCTGCAGCGA	CCCCGCGACC	41820
GAGTCCTTGT	GTGTTCTTTT	TCCCTCCCTC	CCTCCCTCCC	TCCCTCCCTC	CCTCCCTGCT	41880
TCCGAGAGGC	ATCTCCAGAG	ACCGCGCCGT	GGGTGTGCTT	CTGACTCTGT	CGCGGTCGAG	41940
GCAGAGACGC	GTTTTTGGGCA	CCGTTTGTGT	GGGGTGGGGG	CAGAGGGGCT	GCGTTTTCTG	42000
CCTCGGGAAG	AGCTTCTCGA	CTCACGGTTT	CGTTTTCTCG	GTCCACGGGC	CGCCCTGCCA	42060
GCCGGATCTG	TCTCGCTGAC	GTCCGCGGCG	GTTGTGCGGC	TCCATCTGGC	GGCCGCTTTG	42120
AGATCGTGCT	CTCGGCTTCC	GGAGCTGCGG	TGGCAGCTGC	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	ATGCGAGGCT	CCGGAAAGCC	CGCGGTCGTC	AGCCCGGCTG	GCCCGGTGGC	42240
GCCAGAGCTG	TGGCCGGTCG	CTTGTGAGTC	ACAGCTCTGG	CGTGCAGGTT	TATGTGGGGG	42300
AGAGGCTGTC	GCTGCGCTTC	TGGGCCCCCG	GCGGGCGTGG	GGCTGCCCCG	GCCGGTCGAC	42360
CAGCGCGCCG	TAGCTCCCCA	GGCCCCGAGC	GCGACCCGGC	GGACCCGCCG	CGCGTGCGCG	42420

AGGCTGGGGA	CGCCCTTCCC	GGCCCGGTCG	CGGTCCGCTC	ATCCTGGCCG	TCTGAGGCGG	42480
CGGCCGAATT	CGTTTCCGAG	ATCCCCGTGG	GGAGCCGGGG	ACCGTCCCGC	CCCCGTCCCC	42540
CGGGTGCCGG	GGAGCGGTCC	CCGGGCCGGG	CCGCGGTCCC	TCTGCCGCGA	TCCTTTCTGG	42600
CGAGTCCCCG	TGGCCAGTCG	GAGAGCGCTC	CCTGAGCCGG	TGCGGCCCGA	GAGGTCGCGC	42660
TGGCCGGCCT	TCGGTCCCTC	GTGTGTCCCG	GTCGTAGGAG	GGGCCGGCCG	AAAATGCTTC	42720
CGGCTCCCGC	TCTGGAGACA	CGGGCCGGCC	CCTGCGTGTG	GCCAGGGCCG	CCGGGAGGGC	42780
TCCCCGGCCC	GGCGCTGTCC	CCGCGTGTGT	CCTTGGGTTG	ACCAGAGGGA	CCCCGGGCGC	42840
TCCGTGTGTG	GCTGCGATGG	TGGCGTTTTT	GGGGACAGGT	GTCCGTGTCC	GTGTGCGCGC	42900
TCGCCTGGGC	CGGCGGCGTG	GTCGGTGACG	CGACCTCCCC	GCCCCGGGGG	AGGTATATCT	42960
TTCGCTCCGA	GTCGGCAATT	TTGGGCCGCC	GGGTTATAT			42999

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCGCGCG	GGCCCCGTGT	TCGCCGTTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCAGT	GCCGTTGTGG	AGTGCCCTCG	TCTCCTCCTC	CTCCCCGGCA	120
GCGTTCCAC	GGTTGGGGAC	CACCGGTGAC	CTCGCCCTCT	TCGGGCCTGG	ATCCG	175

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGGAAC	GGCGGGGTCG	60
GTCGTGCCCC	GCGCCGGACG	TGTGTGCGGG	CCCACTTCCC	GCTCGAGGGT	GGCGGTGGCG	120
GCGGCGTTGG	TAGTCTCCCG	TGTTGCGTCT	TCCCCGGCTC	TTGGGGGGGG	TGCCGTCGTT	180
TTCGGGGCGG	GCGTTGCTTG	GCTTACGCAG	GCTTGTTTGG	GGACTGCCTC	AGGAGTCGTG	240
GGCGGTGTGA	TTCCCGCCGG	TTTTGCCTCG	CGTCTGCCTG	CTTTGCCTCG	GGTTTGCTTG	300
GTTCGTGTCT	CGGGAGCGGT	GGTTTTTTTT	TTTTTCGGGT	CCCGGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCGTCGCC	CCCTGCCGCC	GGTGGGTTTT	CGTTTCGGGC	TGTGTTTCGTT	420
TCCCTTCCC	CGTTTCGCCG	TCGGTTCTCC	CCGGTCGGTC	GGCCCTCTCC	CCGGTCGGTC	480
GCCCGGCCGT	GCTGCCGGAC	CCCCCTTCT	GGGGGGGATG	CCCGGGCACG	CACGCGTCCG	540
GGCGGCCACT	GTGGTCCGGG	AGCTGCTCGG	CAGGCGGGTG	AGCCAGTTGG	AGGGGCGTCA	600
TGCCCCCGCG	GGCTCCCGTG	GCCGACGCGG	CGTGTTCCTT	GGGGGGGCCT	GTGCGTGCGG	660
GAAGGCTGCG	CACGTTGTCT	GTCCTTGCGA	GGGAAAGAGG	CTTTTTTTTT	TTAGGGGGTC	720
GTCTTTCGTC	GTCCCGTCGG	CGGTGGATCC	GGCCT			755

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAGGTG	CGTCTGCGGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCTCTCCG	GGAAGGCGTT	60
TAGCGGGTAC	CGTCGCCGCG	CCGAGGTGGG	CGCACGTCCG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGGCGGG	GGCTCCGGTC	GATGTCTTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAGCC	TCCGCCTGTG	GGCTTCGTCG	GCCGTCTCCC	CCCCCCTCAC	GTCCCTCGCG	240
AGCGAGCCCG	TCCGTTTCGAC	CTTCCTTCCG	CCTTCCCCCC	ATCTTTCCGC	GCTCCGTTGG	300
CCCCGGGGTT	TTACACGGCG	CCCCACGCT	CCTCCGCCTC	TCCGCCCCGTG	GTTTGGACGC	360
CTGGTTCGG	TCTCCCCGCC	AAACCCCGGT	TGGGTGGTTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGGTCTCCC	AACCCCGGC	CGGAAGGTT	CGGGGGTTCC	GGG		463

- (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCCT	TTCCGGCTCC	GGCCGGGGGG	60
GGCGGCCCCG	GGCGGTTTGG	TGAGTTAGAT	AACCTCGGGC	CGATCGCACG	CCCCCGTGG	120
CGGCGACGAC	CCATTGGAAC	GTCTGCCCTA	TCAACTTTCG	ATGGTAGTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTTCGATTCC	GGAGAGGGAG	CCTGAGAAAC	240
GGCTACCACA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAT	ACAGGACTCT	TTCGAGGCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAAGCAG					378

- (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTCACCGC	CCGTCCCCGC	CCCTTGCTC	TCGGCGCCCC	CTCGATGCTC	180

TTAGCTGAGT	TGTCCCGCGG	GGCCCGAAGC	GTTTACTTTG	AAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCCC	GAGCCGCCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTTTGT	TTGGTTTTTCG	GAAGTGAAGC	CATGATTAAG	GGAAACGGCC	GGGGGCATTC	360
CCTTATTGCG	CCCCCTA					378

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTCC	CGCTCCCCGT	TCCTCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCTTCTTT	60
TCCCCCTCTCC	GGAGGGGGGG	GAGGTGGGGG	CGCGTGGGCG	GGGTCGGGGG	TGGGGTCGGC	120
GGGGGACCGC	CCCCGGCCCG	CAAAAGGCCG	CCGCCGGGCG	CACTTCAACC	GTAGCGGTGC	180
GCCGCGACCG	GCTACGAGAC	GGCTGGGAAG	GCCCCACGGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGCGCC	GAACCACTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCGGGGCC	GAGGGGAAGC	CCGATACCCG	TCGCCGCGCT	TTTCCCCTCC	360
CCCCGTCCGC	CTCCCGGGCG	GGCGTGGGGG	TGGGGGGCCG	GCCGCCCTC	CCACGCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGGC	480
GGACTGTCCCT	CAGTGCGCC	CGGGCGTCGT	CGCGCCGTCG	GGCCCGGGGG	GTTCTCTCGG	540
TCACGCCGCC	CCCGACGAAG	CCGAGCGCAC	GGGGTCGGCG	GCGATGTCGG	CTACCCACCC	600
GACCCGTCTT	GAAACACGGA	CCAAGGAGTC	TAACGCGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCCG	TGGCGCAATG	AAGGTGAAGG	GCCCCGTCCG	GGGGCCCGAG	GTGGGATCC	719

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT	CCAGTCCGCC	GAGGGCGCAC	CACCGGCCCCG	TCTCGCCCCG	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAAGTATGC	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTCGTC	180
CGACCTGGGT	ATAGGGGCGA	AAGACTAATC	GAACCATCTA	GTAAGTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTTATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCCGGA	AACGATCTCA	AACTATTTCT	CAAACTTTAA	360
ATGGGTAAAG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGCG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTTT	GTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTTAAGGCGC	480
CCGATGCCGA	CGCTCATCAG	ACCCAGAAA	AGGTGTTGGT	TGATATAGAC	AGCAGGACGG	540
TGGCCATGGA	AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTCGC	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	CCCCG				685

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG

35

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC

33

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCCTAA CCCTAACCCCT AACCCCTAACC CTAACCCCTAA  
CCCTAACCCCT AACCCGGGAT

60

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21